



SEQUENCE LISTING

<110> Salkoff, Lawrence
Schreiber, Matthew
Silvia, Chris
The Washington University
ICAgene Inc.

<120> A pH Sensitive Potassium Channel in Spermatocytes

<130> 018512-000120US

<140> 09/176,664

<141> 1998-10-21

<150> US 60/063,138

<151> 1997-10-22

<150> US 60/076,172

<151> 1998-02-27

<160> 53

<170> PatentIn Ver. 2.0

<210> 1

<211> 1112

<212> PRT

<213> Mus musculus

BD
<220>

<223> mouse Slo3 (mSlo3)

<220>

<221> VARIANT

<222> (5)

<223> polymorphic variant #2 Leu -> Ile

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<222> (21)

<223> polymorphic variant #1 Ile -> Val

<220>

<221> VARIANT

<222> (25)

<223> polymorphic variant #3 Ala -> Ser

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Thr Ser Cys Thr Ile Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Leu
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Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala
35 40 45

Leu Lys Ser Ser Arg Ser Trp Lys Tyr Val Lys Gly Pro Arg Gly Leu
50 55 60

Leu Glu Leu Phe Ser Ser Arg Arg Ile Glu Ala Asn Pro Leu Arg Lys
 65 70 75 80
 Leu Tyr Phe His Gly Val Phe Arg Gln Arg Ile Glu Met Leu Leu Ser
 85 90 95
 Ala Gln Thr Val Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
 100 105 110
 Ser Ile Gly Ser Leu Val Ile Tyr Phe Ile Asn Ser Met Asp Pro Val
 115 120 125
 Arg Arg Cys Ser Ser Tyr Glu Asp Lys Ile Val His Gly Asp Leu Ser
 130 135 140
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Trp Ala Ala
 145 150 155 160
 Glu Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
 165 170 175
 Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
 180 185 190
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Lys
 195 200 205
 Ile Leu Gln Ile Leu Gln Val Ile Lys Thr Ser Asn Ser Val Lys Leu
 210 215 220
 Ser Lys Leu Leu Ser Ile Val Ile Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Leu His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Asn Gly Arg
 245 250 255
 Asn Ser Gln Thr Met Ser Tyr Phe Glu Ser Ile Tyr Leu Val Thr Ala
 260 265 270
 Thr Met Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
 275 280 285
 Gly Arg Ile Phe Ile Val Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
 290 295 300
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ser Thr Arg Lys Lys
 305 310 315 320
 Tyr Thr Lys Pro Tyr Glu Ala Val Lys Gly Lys Lys Phe Ile Val Val
 325 330 335
 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe
 340 345 350
 Leu His Trp Lys Ser Gly Glu Ile Asn Ile Glu Ile Val Phe Leu Gly
 355 360 365
 Glu Thr Leu Pro Cys Leu Glu Leu Glu Thr Leu Leu Lys Cys His Thr
 370 375 380

Ser Cys Thr Asn Phe Val Cys Gly Thr Ala Leu Lys Phe Glu Asp Leu
 385 390 395 400
 Lys Arg Val Ala Val Glu Asn Ser Glu Ala Cys Leu Ile Leu Ala Asn
 405 410 415
 His Phe Cys Ser Asp Leu His Asp Glu Asp Asn Ser Asn Ile Met Arg
 420 425 430
 Val Leu Ser Ile Lys Asn Tyr Tyr Pro Gln Thr Arg Val Ile Ile Gln
 435 440 445
 Ile Leu Gln Ser Gln Asn Lys Val Phe Leu Ser Lys Ile Pro Asn Trp
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 Asp Trp Ser Ala Gly Asp Asn Ile Leu Cys Phe Ala Glu Leu Lys Leu
 465 470 475 480
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
 485 490 495
 Thr Thr Leu Phe Ile Glu Gln Asn Gln Lys Val Phe Pro Lys His Pro
 500 505 510
 Trp Gln Lys His Phe Leu Asn Gly Leu Lys Asn Lys Ile Leu Thr Gln
 515 520 525
 Arg Leu Ser Asn Asp Phe Val Gly Met Thr Phe Pro Gln Val Ser Arg
 530 535 540
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 545 550 555 560
 Pro Phe Phe His Ser Cys Cys Thr Leu Ile Leu Asn Pro Ser Ser Gln
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 Val Arg Leu Asn Lys Asp Thr Leu Gly Phe Phe Ile Ala Asp Ser Ser
 580 585 590
 Lys Ala Val Lys Arg Ala Phe Phe Tyr Cys Ser Asn Cys His Ser Asp
 595 600 605
 Val Cys Asn Pro Glu Leu Ile Gly Lys Cys Asn Cys Lys Ile Lys Ser
 610 615 620
 Arg Gln Gln Leu Ile Ala Pro Thr Ile Met Val Met Lys Ser Ser Leu
 625 630 635 640
 Thr Asp Phe Thr Thr Ser Ser His Ile His Ala Ser Met Ser Thr Glu
 645 650 655
 Ile His Thr Cys Phe Ser Arg Glu Gln Pro Ser Leu Ile Thr Ile Thr
 660 665 670
 Thr Asn Arg Pro Thr Thr Asn Asp Thr Val Asp Asp Thr Asp Met Leu
 675 680 685
 Asp Ser Ser Gly Met Phe His Trp Cys Arg Ala Met Pro Leu Asp Lys
 690 695 700

Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His
 705 710 715 720
 Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu
 725 730 735
 Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu
 740 745 750
 Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu
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 Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser
 770 775 780
 Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser
 785 790 795 800
 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
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 Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro
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 Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile
 850 855 860
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 Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp
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 Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu
 915 920 925
 Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu
 930 935 940
 Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys
 945 950 955 960
 Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr
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 Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys
 980 985 990
 Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met
 995 1000 1005
 Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr
 1010 1015 1020

Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
1025 1030 1035 1040

Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
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Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg Arg His Trp Pro
1060 1065 1070

Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile
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Pro Glu Ser Ile Leu Trp Thr Arg
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<211> 3339

<212> DNA

<213> Mus musculus

<220>

<223> mouse Slo3 (mSlo3)

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atcttattcc ttttcaagaat agccttggaaa agctcaagaa gttggaaata cgtcaagggg 180
ccaagaggac tcttggaaact attctcatca cgtagaatcg aggctaattcc ttggaggaaa 240
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gtggggcaag tgggggtgat ctttgcgttt gtactaagca tcgggtctct tggatctat 360
ttcatcaatt caatggatcc ttgtcgaagg ttgtttcat atgaagacaa aattgtccat 420
ggggatttga gtttcaacgc tttcttttagc ttctattttgggttggaggtt ttggggcagct 480
gaagacaaga tcaagtctg gttggagatg aattcaattt tagacatccc taccatcccc 540
ccaaaccttta tttcttattt tttgaagatg aattggctag gtttggagatt tctaagagct 600
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aagtgcacca catcctgtac caacttcgtt tgccggaccc cactgaagtt cgaggatctg 1200
aagcgagttt cagttggagaa ctccggcg tgcctgattt tagccacca tttctgttagt 1260
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tttcaagag aacaggctag tttgatcacc attacaacca acagaccaac gacaaacgac 2040
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 aaaacaactc tacaacacgca acgacgccat tggcccgagg gtcgaatttc ttgcattcgc 3240
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 agcaccacca ctcccgagtc tatccttgg acacgttag 3339

<210> 3
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human Slo3-a (hSlo3-a)

<220>
 <221> MOD_RES
 <222> (29)
 <223> Xaa = any amino acid

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Leu Ile Ser Leu Leu Ile Phe Arg Leu Ile Trp Arg Xaa Val Lys Lys
 20 25 30

Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
 35 40 45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
 50 55 60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
 65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
 85 90 95

Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val Gly Thr Leu Phe Ile Ile
 100 105 110

<210> 4
<211> 416
<212> DNA
<213> Homo sapiens

<220>
<223> human Slo3 (hSlo3)

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attatcttgg aactgttcac atcaggtacc atcgcttagga gccatgtaaag aagcctccac 180
ttccaggac aatttcgtga tcatatagaa atgttgctt cagcccagac ctttgtgggg 240
caagtgttgg tgatccttgc ctttgtacta agcattgggt ctcttataat ctatTCatc 300
aattcwgctg accctgttgg aacgctgttc atcatatgaa gacaaaacca ttcctattga 360
tttggttttc aatgcttctt ttagttctt ttttgggttg aggttttggc aaagcc 416

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<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
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<223> mSlo3 peptide starting with amino acid 687

<400> 5
Met Leu Asp Ser
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<210> 6
<211> 112
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> MOD_RES
<222> (29)
<223> Xaa = any amino acid

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Leu Ile Ser Leu Leu Ile Phe Arg Leu Ile Trp Arg Xaa Val Lys Lys
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Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
35 40 45
Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
50 55 60
Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
85 90 95

Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val Gly Thr Leu Phe Ile Ile
100 105 110

<210> 7
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<223> human Slo3-c (hSLO3-c)

<220>
<221> MOD_RES
<222> (29)
<223> Xaa = any amino acid

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Leu Ile Ser Leu Leu Ile Phe Arg Leu Ile Trp Arg Xaa Val Lys Lys
20 25 30

Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
35 40 45

Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
50 55 60

Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
65 70 75 80

Gln Val Leu Val Ile Leu Val Phe Val Leu Ser Ile Gly Ser Leu Ile
85 90 95

Ile Tyr Phe Ile Asn Ser Met Asp Pro Val Gly Thr Leu Phe Ile Ile
100 105 110

<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 primer

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26

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 primer

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28

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 primer

<400> 10
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22

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 primer

<400> 11
tttcaaagcc tcttttagcgg taa

23

<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 primer

<400> 12
ttatgcctgg atctgcactc tacatg

26

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 primer

<400> 13
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23

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hSlo3 primer

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24

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hSlo3 primer

<400> 15
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24

<210> 16
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<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> VARIANT
<222> (6)
<223> polymorphic variant #2 Leu -> Ile

<220>
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<223> polymorphic variant #1 Ile -> Val

<220>
<221> VARIANT
<222> (25)
<223> polymorphic variant #3 Ala -> Ser

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20 25 30

Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Ile Phe Arg Leu Ile
35 40 45

Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
50 55 60

Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
65 70 75 80

Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
85 90 95

Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
 100 105 110
 Ser Ile Gly Ser Leu Ile Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val
 115 120 125
 Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val
 130 135 140
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala
 145 150 155 160
 Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
 165 170 175
 Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
 180 185 190
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Gln
 195 200 205
 Ile Leu Gln Ile Leu Arg Ala Ile Lys Thr Ser Asn Ser Val Lys Phe
 210 215 220
 Ser Lys Leu Leu Ser Ile Ile Leu Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Lys Gly Arg
 245 250 255
 Asn Ser Gln Asn Ile Ser Tyr Phe Glu Ser Ile Tyr Leu Val Met Ala
 260 265 270
 Thr Thr Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
 275 280 285
 Gly Arg Thr Phe Ile Met Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
 290 295 300
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ala Asn Lys Arg Lys
 305 310 315 320
 Tyr Thr Ser Ser Tyr Glu Ala Leu Lys Gly Lys Lys Phe Ile Val Val
 325 330 335
 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe
 340 345 350
 Leu Arg Asp Lys Ser Gly Glu Ile Asn Thr Glu Ile Val Phe Leu Gly
 355 360 365
 Glu Thr Pro Pro Ser Leu Glu Leu Glu Thr Ile Phe Lys Cys Tyr Leu
 370 375 380
 Ala Tyr Thr Thr Phe Ile Ser Gly Ser Ala Met Lys Trp Glu Asp Leu
 385 390 395 400
 Arg Arg Val Ala Val Glu Ser Ala Glu Ala Cys Leu Ile Ile Ala Asn
 405 410 415

Pro Leu Cys Ser Asp Ser His Ala Glu Asp Ile Ser Asn Ile Met Arg
 420 425 430
 Val Leu Ser Ile Lys Asn Tyr Asp Ser Thr Thr Arg Ile Ile Ile Gln
 435 440 445
 Ile Leu Gln Ser His Asn Lys Val Tyr Leu Pro Lys Ile Pro Ser Trp
 450 455 460
 Asn Trp Asp Thr Gly Asp Asn Ile Ile Cys Phe Ala Glu Leu Lys Leu
 465 470 475 480
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
 485 490 495
 Thr Ser Leu Phe Val Glu Gln Asn Lys Lys Val Met Pro Lys Gln Thr
 500 505 510
 Trp Lys Lys His Phe Leu Asn Ser Met Lys Asn Lys Ile Leu Thr Gln
 515 520 525
 Arg Leu Ser Asp Asp Phe Ala Gly Met Ser Phe Pro Glu Val Ala Arg
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 Leu Cys Phe Leu Lys Met Tyr Leu Leu Leu Ile Ala Ile Glu Tyr Lys
 545 550 555 560
 Ser Leu Phe Thr Asp Gly Phe Cys Gly Leu Ile Leu Asn Pro Pro Pro
 565 570 575
 Gln Val Arg Ile Arg Lys Asn Thr Leu Gly Phe Phe Ile Ala Glu Thr
 580 585 590
 Pro Lys Asp Val Arg Arg Ala Leu Phe Tyr Cys Ser Val Cys His Asp
 595 600 605
 Asp Val Phe Ile Pro Glu Leu Ile Thr Asn Cys Gly Cys Lys Ser Arg
 610 615 620
 Ser Arg Gln His Ile Thr Val Pro Ser Val Lys Arg Met Lys Lys Cys
 625 630 635 640
 Leu Lys Gly Ile Ser Ser Arg Ile Ser Gly Gln Asp Ser Pro Pro Arg
 645 650 655
 Val Ser Ala Ser Thr Ser Ser Ile Ser Asn Phe Thr Thr Arg Thr Leu
 660 665 670
 Gln His Asp Val Glu Gln Asp Ser Asp Gln Leu Asp Ser Ser Gly Met
 675 680 685
 Phe His Trp Cys Lys Pro Thr Ser Leu Asp Lys Val Thr Leu Lys Arg
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 Thr Gly Lys Ser Lys Tyr Lys Phe Arg Asn His Ile Val Ala Cys Val
 705 710 715 720
 Phe Gly Asp Ala His Ser Ala Pro Met Gly Leu Arg Asn Phe Val Met
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Pro Leu Arg Ala Ser Asn Tyr Thr Arg Lys Glu Leu Lys Asp Ile Val
 740 745 750
 Phe Ile Gly Ser Leu Asp Tyr Leu Gln Arg Glu Trp Arg Phe Leu Arg
 755 760 765
 Asn Phe Pro Gln Ile Tyr Ile Leu Pro Gly Cys Ala Leu Tyr Ser Gly
 770 775 780
 Asp Leu His Ala Ala Asn Ile Glu Gln Cys Ser Met Cys Ala Val Leu
 785 790 795 800
 Ser Pro Pro Pro Gln Pro Ser Ser Asn Gln Thr Leu Val Asp Thr Glu
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 Ala Ile Met Ala Thr Leu Thr Ile Gly Ser Leu Gln Ile Asp Ser Ser
 820 825 830
 Ser Asp Pro Ser Pro Ser Val Ser Glu Glu Thr Pro Gly Tyr Thr Asn
 835 840 845
 Gly His Asn Glu Lys Ser Asn Cys Arg Lys Val Pro Ile Leu Thr Glu
 850 855 860
 Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu Gln Leu Gly Gly Leu
 865 870 875 880
 Glu Gly Ser Leu Gln Glu Thr Asn Leu His Leu Ser Thr Ala Phe Ser
 885 890 895
 Thr Gly Thr Val Phe Ser Ser Ser Phe Leu Asp Ser Leu Leu Ala Thr
 900 905 910
 Ala Phe Tyr Asn Tyr His Val Leu Glu Leu Leu Gln Met Leu Val Thr
 915 920 925
 Gly Gly Val Ser Ser Gln Leu Glu Gln His Leu Asp Lys Asp Lys Val
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 Tyr Gly Val Ala Asp Ser Cys Thr Ser Leu Leu Ser Gly Arg Asn Arg
 945 950 955 960
 Cys Lys Leu Gly Leu Leu Ser Leu His Glu Thr Ile Leu Ser Asp Val
 965 970 975
 Asn Pro Arg Asn Thr Phe Gly Gln Leu Phe Cys Gly Ser Leu Asp Leu
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 Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Ile Ile Asp Glu Glu Glu
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 Thr Ala Cys Tyr Lys Arg Asn Glu Glu Phe Ser Leu Gln Lys Ser Tyr
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Glu Ile Val Asn Lys Ala Ser Gln Thr Thr Glu Asp Thr Phe Arg His
1060 1065 1070

Lys Leu Ser Ser His Pro Leu Ile Gln Leu Leu Arg His Cys Ile His
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Gln Ser Ile Leu Thr Ser Arg Glu Leu Thr Pro Ser Leu Phe Leu Ser
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Lys
1105

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<212> DNA
<213> Homo sapiens

<220>
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> human hSlo3-2 (hSlo3-2)

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 Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Ile Phe Arg Leu Ile
 35 40 45
 Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
 50 55 60
 Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
 65 70 75 80
 Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
 85 90 95
 Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
 100 105 110
 Ser Ile Gly Ser Leu Ile Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val
 115 120 125
 Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val
 130 135 140
 Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala
 145 150 155 160
 Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
 165 170 175

Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
 180 185 190
 Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Gln
 195 200 205
 Ile Leu Gln Ile Leu Arg Ala Ile Lys Thr Ser Asn Ser Val Lys Phe
 210 215 220
 Ser Lys Leu Leu Ser Ile Ile Leu Ser Thr Trp Phe Thr Ala Ala Gly
 225 230 235 240
 Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Lys Gly Arg
 245 250 255
 Asn Ser Gln Asn Ile Ser Tyr Phe Glu Ser Ile Tyr Leu Val Met Ala
 260 265 270
 Thr Thr Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
 275 280 285
 Gly Arg Thr Phe Ile Met Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
 290 295 300
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ala Asn Lys Arg Lys
 305 310 315 320
 Tyr Thr Ser Ser Tyr Glu Ala Leu Lys Gly Lys Lys Phe Ile Val Val
 325 330 335
 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe
 340 345 350
 Leu Arg Asp Lys Ser Gly Glu Ile Asn Thr Glu Ile Val Phe Leu Gly
 355 360 365
 Glu Thr Pro Pro Ser Leu Glu Leu Glu Thr Ile Phe Lys Cys Tyr Leu
 370 375 380
 Ala Tyr Thr Thr Phe Ile Ser Gly Ser Ala Met Lys Trp Glu Asp Leu
 385 390 395 400
 Arg Arg Val Ala Val Glu Ser Ala Glu Ala Cys Leu Ile Ile Ala Asn
 405 410 415
 Pro Leu Cys Ser Asp Ser His Ala Glu Asp Ile Ser Asn Ile Met Arg
 420 425 430
 Val Leu Ser Ile Lys Asn Tyr Asp Ser Thr Thr Arg Ile Ile Ile Gln
 435 440 445
 Ile Leu Gln Ser His Asn Lys Val Tyr Leu Pro Lys Ile Pro Ser Trp
 450 455 460
 Asn Trp Asp Thr Gly Asp Asn Ile Ile Cys Phe Ala Glu Leu Lys Leu
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 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
 485 490 495

Thr Ser Leu Phe Val Glu Gln Asn Lys Lys Val Met Pro Lys Gln Thr
 500 505 510
 Trp Lys Lys His Phe Leu Asn Ser Met Lys Asn Lys Ile Leu Thr Gln
 515 520 525
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 530 535 540
 Gly Leu Ile Leu Asn Pro Pro Gln Val Arg Ile Arg Lys Asn Thr
 545 550 555 560
 Leu Gly Phe Phe Ile Ala Glu Thr Pro Lys Asp Val Arg Arg Ala Leu
 565 570 575
 Phe Tyr Cys Ser Val Cys His Asp Asp Val Phe Ile Pro Glu Leu Ile
 580 585 590
 Thr Asn Cys Gly Cys Lys Ser Arg Ser Arg Gln His Ile Thr Val Pro
 595 600 605
 Ser Val Lys Arg Met Lys Lys Cys Leu Lys Gly Ile Ser Ser Arg Ile
 610 615 620
 Ser Gly Gln Asp Ser Pro Pro Arg Val Ser Ala Ser Thr Ser Ser Ile
 625 630 635 640
 Ser Asn Phe Thr Thr Arg Thr Leu Gln His Asp Val Glu Gln Asp Ser
 645 650 655
 Asp Gln Leu Asp Ser Ser Gly Met Phe His Trp Cys Lys Pro Thr Ser
 660 665 670
 Leu Asp Lys Val Thr Leu Lys Arg Thr Gly Lys Ser Lys Tyr Lys Phe
 675 680 685
 Arg Asn His Ile Val Ala Cys Val Phe Gly Asp Ala His Ser Ala Pro
 690 695 700
 Met Gly Leu Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr
 705 710 715 720
 Arg Lys Glu Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Asp Tyr Leu
 725 730 735
 Gln Arg Glu Trp Arg Phe Leu Arg Asn Phe Pro Gln Ile Tyr Ile Leu
 740 745 750
 Pro Gly Cys Ala Leu Tyr Ser Gly Asp Leu His Ala Ala Asn Ile Glu
 755 760 765
 Gln Cys Ser Met Cys Ala Val Leu Ser Pro Pro Gln Pro Ser Ser
 770 775 780
 Asn Gln Thr Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Thr Ile
 785 790 795 800
 Gly Ser Leu Gln Ile Asp Ser Ser Asp Pro Ser Pro Ser Val Ser
 805 810 815

Glu Glu Thr Pro Gly Tyr Thr Asn Gly His Asn Glu Lys Ser Asn Cys
 820 825 830
 Arg Lys Val Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His
 835 840 845
 Phe Ile Glu Gln Leu Gly Gly Leu Glu Gly Ser Leu Gln Glu Thr Asn
 850 855 860
 Leu His Leu Ser Thr Ala Phe Ser Thr Gly Thr Val Phe Ser Ser Ser
 865 870 875 880
 Phe Leu Asp Ser Leu Leu Ala Thr Ala Phe Tyr Asn Tyr His Val Leu
 885 890 895
 Glu Leu Leu Gln Met Leu Val Thr Gly Gly Val Ser Ser Gln Leu Glu
 900 905 910
 Gln His Leu Asp Lys Asp Lys Val Tyr Gly Val Ala Asp Ser Cys Thr
 915 920 925
 Ser Leu Leu Ser Gly Arg Asn Arg Cys Lys Leu Gly Leu Leu Ser Leu
 930 935 940
 His Glu Thr Ile Leu Ser Asp Val Asn Pro Arg Asn Thr Phe Gly Gln
 945 950 955 960
 Leu Phe Cys Gly Ser Leu Asp Leu Phe Gly Ile Leu Cys Val Gly Leu
 965 970 975
 Tyr Arg Ile Ile Asp Glu Glu Leu Asn Pro Glu Asn Lys Arg Phe
 980 985 990
 Val Ile Thr Arg Pro Ala Asn Glu Phe Lys Leu Leu Pro Ser Asp Leu
 995 1000 1005
 Val Phe Cys Ala Ile Pro Phe Ser Thr Ala Cys Tyr Lys Arg Asn Glu
 1010 1015 1020
 Glu Phe Ser Leu Gln Lys Ser Tyr Glu Ile Val Asn Lys Ala Ser Gln
 1025 1030 1035 1040
 Thr Thr Glu Asp Thr Phe Arg His Lys Leu Ser Ser His Pro Leu Ile
 1045 1050 1055
 Gln Leu Leu Arg His Cys Ile His Gln Ser Ile Leu Thr Ser Arg Glu
 1060 1065 1070
 Leu Thr Pro Ser Leu Phe Leu Ser Lys
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 <212> DNA
 <213> Homo sapiens

<220>
 <223> human Slo3-2 (hSlo3-2)

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acaggaatta ttttggaaact gttcacatca ggtaccatcg cttaggagcca tgtaagaagc 240
ctccacattcc agggacaatt tcgtgatcat ctttgcattt atagaaatgt tgcttcagc ccagacctt 300
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<212> PRT
<213> *Mus musculus*

<220>
<223> mouse Slo3 (mSlo3)

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Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala
35 40 45
Leu Lys Ser Ser Arg Ser Trp Lys Tyr Val Lys Gly Pro Arg Gly Leu
50 55 60
Leu Glu Leu Phe Ser Ser Arg Arg Ile Glu Ala Asn Pro Leu Arg Lys
65 70 75 80
Leu Tyr Phe His Gly Val Phe Arg Gln Arg Ile Glu Met Leu Leu Ser
85 90 95
Ala Gln Thr Val Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
100 105 110
Ser Ile Gly Ser Leu Val Ile Tyr Phe Ile Asn Ser Met Asp Pro Val
115 120 125
Arg Arg Cys Ser Ser Tyr Glu Asp Lys Ile Val His Gly Asp Leu Ser
130 135 140
Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Trp Ala Ala
145 150 155 160
Glu Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
165 170 175
Phe Thr Ile Pro Pro Thr Phe Ile Ser Tyr Tyr Leu Lys Ser Asn Trp
180 185 190
Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Leu Glu Leu Pro Lys
195 200 205
Ile Leu Gln Ile Leu Gln Val Ile Lys Thr Ser Asn Ser Val Lys Leu
210 215 220
Ser Lys Leu Leu Ser Ile Val Ile Ser Thr Trp Phe Thr Ala Ala Gly
225 230 235 240
Phe Leu His Leu Val Glu Asn Ser Gly Asp Pro Trp Leu Asn Gly Arg
245 250 255
Asn Ser Gln Thr Met Ser Tyr Phe Glu Ser Ile Tyr Leu Val Thr Ala
260 265 270

Thr Met Ser Thr Val Gly Phe Gly Asp Val Val Ala Lys Thr Ser Leu
 275 280 285
 Gly Arg Ile Phe Ile Val Phe Phe Thr Leu Gly Ser Leu Ile Leu Phe
 290 295 300
 Ala Asn Tyr Ile Pro Glu Met Val Glu Leu Phe Ser Thr Arg Lys Lys
 305 310 315 320
 Tyr Thr Lys Pro Tyr Glu Ala Val Lys Gly Lys Lys Phe Ile Val Val
 325 330 335
 Cys Gly Asn Ile Thr Val Asp Ser Val Thr Ala Phe Leu Arg Asn Phe
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 355 360 365
 Glu Thr Leu Pro Cys Leu Glu Leu Glu Thr Leu Leu Lys Cys His Thr
 370 375 380
 Ser Cys Thr Asn Phe Val Cys Gly Thr Ala Leu Lys Phe Glu Asp Leu
 385 390 395 400
 Lys Arg Val Ala Val Glu Asn Ser Glu Ala Cys Leu Ile Leu Ala Asn
 405 410 415
 His Phe Cys Ser Asp Leu His Asp Glu Asp Asn Ser Asn Ile Met Arg
 420 425 430
 Val Leu Ser Ile Lys Asn Tyr Tyr Pro Gln Thr Arg Val Ile Ile Gln
 435 440 445
 Ile Leu Gln Ser Gln Asn Lys Val Phe Leu Ser Lys Ile Pro Asn Trp
 450 455 460
 Asp Trp Ser Ala Gly Asp Asn Ile Leu Cys Phe Ala Glu Leu Lys Leu
 465 470 475 480
 Gly Phe Ile Ala Gln Gly Cys Leu Val Pro Gly Leu Cys Thr Phe Leu
 485 490 495
 Thr Thr Leu Phe Ile Glu Gln Asn Gln Lys Val Phe Pro Lys His Pro
 500 505 510
 Trp Gln Lys His Phe Leu Asn Gly Leu Lys Asn Lys Ile Leu Thr Gln
 515 520 525
 Arg Leu Ser Asn Asp Phe Val Gly Met Thr Phe Pro Gln Val Ser Arg
 530 535 540
 Leu Cys Phe Val Lys Leu Asn Leu Met Leu Ile Ala Ile Gln His Lys
 545 550 555 560
 Pro Phe Phe His Ser Cys Cys Thr Leu Ile Leu Asn Pro Ser Ser Gln
 565 570 575
 Val Arg Leu Asn Lys Asp Thr Leu Gly Phe Phe Ile Ala Asp Ser Ser
 580 585 590

Lys Ala Val Lys Arg Ala Phe Phe Tyr Cys Ser Asn Cys His Ser Asp
 595 600 605
 Val Cys Asn Pro Glu Leu Ile Gly Lys Cys Asn Cys Lys Ile Lys Ser
 610 615 620
 Arg Gln Gln Leu Ile Ala Pro Thr Ile Met Val Met Lys Ser Ser Leu
 625 630 635 640
 Thr Asp Phe Thr Thr Ser Ser His Ile His Ala Ser Met Ser Thr Glu
 645 650 655
 Ile His Thr Cys Phe Ser Arg Glu Gln Pro Ser Leu Ile Thr Ile Thr
 660 665 670
 Thr Asn Arg Pro Thr Thr Asn Asp Thr Val Asp Asp Thr Asp Met Leu
 675 680 685
 Asp Ser Ser Gly Met Phe His Trp Cys Arg Ala Met Pro Leu Asp Lys
 690 695 700
 Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His
 705 710 715 720
 Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu
 725 730 735
 Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu
 740 745 750
 Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu
 755 760 765
 Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser
 770 775 780
 Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser
 785 790 795 800
 Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
 805 810 815
 Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Asn Ile Gln Ser Leu
 820 825 830
 Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro
 835 840 845
 Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile
 850 855 860
 Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu
 865 870 875 880
 Gln Met Gly Gly Leu Asp Gly Met Leu Lys Gly Thr Ser Leu His Leu
 885 890 895
 Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp
 900 905 910

Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu
 915 920 925
 Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu
 930 935 940
 Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys
 945 950 955 960
 Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr
 965 970 975
 Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys
 980 985 990
 Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met
 995 1000 1005
 Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr
 1010 1015 1020
 Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
 1025 1030 1035 1040
 Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
 1045 1050 1055
 Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg Arg His Trp Pro
 1060 1065 1070
 Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile
 1075 1080 1085
 Phe Thr Gln Ser Thr Thr Arg Glu Arg Gly Gly Leu Ser Thr Thr Thr
 1090 1095 1100
 Pro Glu Ser Ile Leu Trp Thr Arg Gln Leu Phe Cys Gly Ser Leu Asp
 1105 1110 1115 1120
 Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met Ile Asp
 1125 1130

<210> 21
 <211> 1236
 <212> PRT
 <213> Mus musculus

 <220>
 <223> mouse Slol (mSlol)

<400> 21
 Met Asp Ala Leu Ile Ile Pro Val Thr Met Glu Val Pro Cys Asp Ser
 1 5 10 15
 Arg Gly Gln Arg Met Trp Trp Ala Phe Leu Ala Ser Ser Met Val Thr
 20 25 30
 Phe Phe Gly Gly Leu Phe Ile Leu Leu Trp Arg Thr Leu Lys Tyr
 35 40 45

Leu Trp Thr Val Cys Cys His Cys Gly Gly Lys Thr Lys Glu Ala Gln
 50 55 60

Lys Ile Asn Asn Gly Ser Ser Gln Ala Asp Gly Thr Leu Lys Pro Val
 65 70 75 80

Asp Glu Lys Glu Glu Val Val Ala Ala Glu Val Gly Trp Met Thr Ser
 85 90 95

Val Lys Asp Trp Ala Gly Val Met Ile Ser Ala Gln Thr Leu Thr Gly
 100 105 110

Arg Val Leu Val Val Leu Val Phe Ala Leu Ser Ile Gly Ala Leu Val
 115 120 125

Ile Tyr Phe Ile Asp Ser Ser Asn Pro Ile Glu Ser Cys Gln Asn Phe
 130 135 140

Tyr Lys Asp Phe Thr Leu Gln Ile Asp Met Ala Phe Asn Val Phe
 145 150 155 160

Leu Leu Tyr Phe Gly Leu Arg Phe Ile Ala Ala Asn Asp Lys Leu Trp
 165 170 175

Phe Trp Leu Glu Val Asn Ser Val Val Asp Phe Phe Thr Val Pro Pro
 180 185 190

Val Phe Val Ser Val Tyr Leu Asn Arg Ser Trp Leu Gly Leu Arg Phe
 195 200 205

Leu Arg Ala Leu Arg Leu Ile Gln Phe Ser Glu Ile Leu Gln Phe Leu
 210 215 220

Asn Ile Leu Lys Thr Ser Asn Ser Ile Lys Leu Val Asn Leu Leu Ser
 225 230 235 240

Ile Phe Ile Ser Thr Trp Leu Thr Ala Ala Gly Phe Ile His Leu Val
 245 250 255

Glu Asn Ser Gly Asp Pro Trp Glu Asn Phe Gln Asn Asn Gln Ala Leu
 260 265 270

Thr Tyr Trp Glu Cys Val Tyr Leu Leu Met Val Thr Met Ser Thr Val
 275 280 285

Gly Tyr Gly Asp Val Tyr Ala Lys Thr Thr Leu Gly Arg Leu Phe Met
 290 295 300

Val Phe Phe Ile Leu Gly Gly Leu Ala Met Phe Ala Ser Tyr Val Pro
 305 310 315 320

Glu Ile Ile Glu Leu Ile Gly Asn Arg Lys Lys Tyr Gly Gly Ser Tyr
 325 330 335

Ser Ala Val Ser Gly Arg Lys His Ile Val Val Cys Gly His Ile Thr
 340 345 350

Leu Glu Ser Val Ser Asn Phe Leu Lys Asp Phe Leu His Lys Asp Arg
 355 360 365

Asp Asp Val Asn Val Glu Ile Val Phe Leu His Asn Ile Ser Pro Asn
 370 375 380
 Leu Glu Leu Glu Ala Leu Phe Lys Arg His Phe Thr Gln Val Glu Phe
 385 390 395 400
 Tyr Gin Gly Ser Val Leu Asn Pro His Asp Leu Ala Arg Val Lys Ile
 405 410 415
 Glu Ser Ala Asp Ala Cys Leu Ile Leu Ala Asn Lys Tyr Cys Ala Asp
 420 425 430
 Pro Asp Ala Glu Asp Ala Ser Asn Ile Met Arg Val Ile Ser Ile Lys
 435 440 445
 Asn Tyr His Pro Lys Ile Arg Ile Ile Thr Gln Met Leu Gln Tyr His
 450 455 460
 Asn Lys Ala His Leu Leu Asn Ile Pro Ser Trp Asn Trp Lys Glu Gly
 465 470 475 480
 Asp Asp Ala Ile Cys Leu Ala Glu Leu Lys Leu Gly Phe Ile Ala Gln
 485 490 495
 Ser Cys Leu Ala Gln Gly Leu Ser Thr Met Leu Ala Asn Leu Phe Ser
 500 505 510
 Met Arg Ser Phe Ile Lys Ile Glu Glu Asp Thr Trp Gln Lys Tyr Tyr
 515 520 525
 Leu Glu Gly Val Ser Asn Glu Met Tyr Thr Glu Tyr Leu Ser Ser Ala
 530 535 540
 Phe Val Gly Leu Ser Phe Pro Thr Val Cys Glu Leu Cys Phe Val Lys
 545 550 555 560
 Leu Lys Leu Leu Met Ile Ala Ile Glu Tyr Lys Ser Ala Asn Arg Glu
 565 570 575
 Ser Arg Ile Leu Ile Asn Pro Gly Asn His Leu Lys Ile Gln Glu Gly
 580 585 590
 Thr Leu Gly Phe Phe Ile Ala Ser Asp Ala Lys Glu Val Lys Arg Ala
 595 600 605
 Phe Phe Tyr Cys Lys Ala Cys His Asp Asp Val Thr Asp Pro Lys Arg
 610 615 620
 Ile Lys Lys Cys Gly Cys Arg Arg Leu Ile Tyr Phe Glu Asp Glu Gln
 625 630 635 640
 Pro Pro Thr Leu Ser Pro Lys Lys Gln Arg Asn Gly Gly Met Arg
 645 650 655
 Asn Ser Pro Asn Thr Ser Pro Lys Leu Met Arg His Asp Pro Leu Leu
 660 665 670
 Ile Pro Gly Asn Asp Gln Ile Asp Asn Met Asp Ser Asn Val Lys Lys
 675 680 685

Tyr Asp Ser Thr Gly Met Phe His Trp Cys Ala Pro Lys Glu Ile Glu
 690 695 700
 Lys Val Ile Leu Thr Arg Ser Glu Ala Ala Met Thr Val Leu Ser Gly
 705 710 715 720
 His Val Val Val Cys Ile Phe Gly Asp Val Ser Ser Ala Leu Ile Gly
 725 730 735
 Leu Arg Asn Leu Val Met Pro Leu Arg Ala Ser Asn Phe His Tyr His
 740 745 750
 Glu Leu Lys His Ile Val Phe Val Gly Ser Ile Glu Tyr Leu Lys Arg
 755 760 765
 Glu Trp Glu Thr Leu His Asn Phe Pro Lys Val Ser Ile Leu Pro Gly
 770 775 780
 Thr Pro Leu Ser Arg Ala Asp Leu Arg Ala Val Asn Ile Asn Leu Cys
 785 790 795 800
 Asp Met Cys Val Ile Leu Ser Ala Asn Gln Asn Asn Ile Asp Asp Thr
 805 810 815
 Ser Leu Gln Asp Lys Glu Cys Ile Leu Ala Ser Leu Asn Ile Lys Ser
 820 825 830
 Met Gln Phe Asp Asp Ser Ile Gly Val Leu Gln Ala Asn Ser Gln Gly
 835 840 845
 Phe Thr Pro Pro Gly Met Asp Arg Ser Ser Pro Asp Asn Ser Pro Val
 850 855 860
 His Gly Met Leu Arg Gln Pro Ser Ile Thr Thr Gly Val Asn Ile Pro
 865 870 875 880
 Ile Ile Thr Glu Leu Val Asn Asp Thr Asn Val Gln Phe Leu Asp Gln
 885 890 895
 Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu Tyr Leu Thr Gln Pro Phe
 900 905 910
 Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser
 915 920 925
 Ala Thr Tyr Phe Asn Asp Asn Ile Leu Thr Leu Ile Arg Thr Leu Val
 930 935 940
 Thr Gly Gly Ala Thr Pro Glu Leu Glu Ala Leu Ile Ala Glu Glu Asn
 945 950 955 960
 Ala Leu Arg Gly Gly Tyr Ser Thr Pro Gln Thr Leu Ala Asn Arg Asp
 965 970 975
 Arg Cys Arg Val Ala Gln Leu Ala Leu Leu Asp Gly Pro Phe Ala Asp
 980 985 990
 Leu Gly Asp Gly Gly Cys Tyr Gly Asp Leu Phe Cys Lys Ala Leu Lys
 995 1000 1005

Thr Tyr Asn Met Leu Cys Phe Gly Ile Tyr Arg Leu Arg Asp Ala His
 1010 1015 1020
 Leu Ser Thr Pro Ser Gln Cys Thr Lys Arg Tyr Val Ile Thr Asn Pro
 1025 1030 1035 1040
 Pro Tyr Glu Phe Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met
 1045 1050 1055
 Gln Phe Asp His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser
 1060 1065 1070
 Ser His Ser Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser
 1075 1080 1085
 Ile Pro Ser Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser
 1090 1095 1100
 Arg Asp Lys Gln Asn Ala Thr Arg Met Thr Arg Met Gly Gln Ala Glu
 1105 1110 1115 1120
 Lys Lys Trp Phe Thr Asp Glu Pro Asp Asn Ala Tyr Pro Arg Asn Ile
 1125 1130 1135
 Gln Ile Lys Pro Met Ser Thr His Met Ala Asn Gln Ile Asn Gln Tyr
 1140 1145 1150
 Lys Ser Thr Ser Ser Leu Ile Pro Pro Ile Arg Glu Val Glu Asp Glu
 1155 1160 1165
 Cys Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met Gln Phe Asp
 1170 1175 1180
 His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser Ser His Ser
 1185 1190 1195 1200
 Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser Ile Pro Ser
 1205 1210 1215
 Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser Arg Asp Lys
 1220 1225 1230
 Gln Asn Ala Thr
 1235

 <210> 22
 <211> 1262
 <212> PRT
 <213> Drosophila sp.

 <220>
 <223> Drosophila Slo1 (dSlo1)

 <400> 22
 Met Ala Ser Gly Leu Ile Asp Thr Asn Phe Ser Ser Thr Leu Ala Asn
 1 5 10 15
 Gly Met Ser Gly Cys Asp Gln Ser Thr Val Glu Pro Leu Ala Asp Asp
 20 25 30

Pro Thr Asp Ser Pro Phe Asp Ala Asp Asp Cys Leu Lys Val Arg Lys
 35 40 45
 Tyr Trp Cys Phe Leu Leu Ser Ser Ile Phe Thr Phe Leu Ala Gly Leu
 50 55 60
 Leu Val Val Leu Leu Trp Arg Ala Phe Ala Phe Val Ser Cys Arg Lys
 65 70 75 80
 Glu Pro Asp Leu Gly Pro Asn Asp Pro Lys Gln Lys Glu Gln Lys Ala
 85 90 95
 Ser Arg Asn Lys Gln Glu Phe Glu Gly Thr Phe Met Thr Glu Ala Lys
 100 105 110
 Asp Trp Ala Gly Glu Leu Ile Ser Gly Gln Thr Thr Thr Gly Arg Ile
 115 120 125
 Leu Val Val Leu Val Phe Ile Leu Ser Ile Ala Ser Leu Ile Ile Tyr
 130 135 140
 Phe Val Asp Ala Ser Ser Glu Glu Val Glu Arg Cys Gln Lys Trp Ser
 145 150 155 160
 Asn Asn Ile Thr Gln Gln Ile Asp Leu Ala Phe Asn Ile Phe Phe Met
 165 170 175
 Val Tyr Phe Phe Ile Arg Phe Ile Ala Ala Ser Asp Lys Leu Trp Phe
 180 185 190
 Met Leu Glu Met Tyr Ser Phe Val Asp Tyr Phe Thr Ile Pro Pro Ser
 195 200 205
 Phe Val Ser Ile Tyr Leu Asp Arg Thr Trp Ile Gly Leu Arg Phe Leu
 210 215 220
 Arg Ala Leu Arg Leu Met Thr Val Pro Asp Ile Leu Gln Tyr Leu Asn
 225 230 235 240
 Val Leu Lys Thr Ser Ser Ile Arg Leu Ala Gln Leu Val Ser Ile
 245 250 255
 Phe Ile Ser Val Trp Leu Thr Ala Ala Gly Ile Ile His Leu Leu Glu
 260 265 270
 Asn Ser Gly Asp Pro Leu Asp Phe Asn Asn Ala His Arg Leu Ser Tyr
 275 280 285
 Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly Tyr
 290 295 300
 Gly Asp Val Tyr Cys Glu Thr Val Leu Gly Arg Thr Phe Leu Val Phe
 305 310 315 320
 Phe Leu Leu Val Gly Leu Ala Val Phe Ala Ser Trp Ile Pro Glu Ile
 325 330 335
 Thr Glu Leu Ala Ala Gln Arg Ser Lys Tyr Gly Gly Thr Tyr Ser Lys
 340 345 350

Asp Pro Arg Lys Arg His Ile Val Val Cys Gly His Ile Thr Tyr Glu
 355 360 365
 Ser Val Ser His Phe Leu Lys Asp Phe Leu His Glu Asp Arg Glu Asp
 370 375 380
 Val Asp Val Glu Val Val Phe Leu His Arg Lys Pro Pro Asp Leu Glu
 385 390 395 400
 Leu Glu Gly Leu Phe Lys Arg His Phe Thr Thr Val Glu Phe Phe Gln
 405 410 415
 Gly Thr Ile Met Asn Pro Ile Asp Leu Gln Arg Val Lys Val His Glu
 420 425 430
 Ala Asp Ala Cys Leu Val Leu Ala Asn Lys Tyr Cys Gln Asp Pro Asp
 435 440 445
 Ala Glu Asp Ala Ala Asn Ile Met Arg Val Ile Ser Ile Lys Asn Tyr
 450 455 460
 Ser Asp Asp Ile Arg Val Ile Ile Gln Leu Met Gln Tyr His Asn Lys
 465 470 475 480
 Ala Tyr Leu Leu Asn Ile Pro Ser Trp Asp Trp Lys Gln Gly Asp Asp
 485 490 495
 Val Ile Cys Leu Ala Glu Leu Lys Leu Gly Phe Ile Ala Gln Ser Cys
 500 505 510
 Leu Ala Pro Gly Phe Ser Thr Met Met Ala Asn Leu Phe Ala Met Arg
 515 520 525
 Ser Phe Lys Thr Ser Pro Asp Met Gln Ser Trp Thr Asn Asp Tyr Leu
 530 535 540
 Arg Gly Thr Gly Met Glu Met Tyr Thr Glu Thr Leu Ser Pro Thr Phe
 545 550 555 560
 Ile Gly Ile Pro Phe Ala Gln Ala Thr Glu Leu Cys Phe Ser Lys Leu
 565 570 575
 Lys Leu Leu Leu Leu Ala Ile Glu Ile Lys Gly Ala Glu Glu Gly Ala
 580 585 590
 Asp Ser Lys Ile Ser Ile Asn Pro Arg Gly Ala Lys Ile Gln Ala Asn
 595 600 605
 Thr Gln Gly Phe Phe Ile Ala Gln Ser Ala Asp Glu Val Lys Arg Ala
 610 615 620
 Trp Phe Tyr Cys Lys Ala Cys His Glu Asp Ile Lys Asp Glu Thr Leu
 625 630 635 640
 Ile Lys Lys Cys Lys Cys Lys Asn Leu Thr Val Gln Pro Arg Ser Lys
 645 650 655
 Phe Asp Asp Leu Gly Asp Ile Thr Arg Asp Arg Glu Asp Thr Asn Leu
 660 665 670

Leu Asn Arg Asn Val Arg Arg Pro Asn Gly Thr Gly Asn Gly Thr Gly
 675 680 685
 Gly Met His His Met Asn Ser Thr Arg Ala Ala Ala Ala Ala Ala
 690 695 700
 Ala Ala Gly Lys Gln Val Asn Lys Val Lys Pro Thr Val Asn Val Ser
 705 710 715 720
 Arg Gln Val Glu Gly Gln Val Ile Ser Pro Ser Gln Tyr Asn Arg Pro
 725 730 735
 Thr Ser Arg Ser Ser Gly Thr Gly Thr Gln Asn Gln Asn Gly Gly Val
 740 745 750
 Ser Leu Pro Ala Gly Ile Ala Asp Asp Gln Ser Lys Asp Phe Asp Phe
 755 760 765
 Glu Lys Thr Glu Met Lys Tyr Asp Ser Thr Gly Met Phe His Trp Ser
 770 775 780
 Pro Ala Lys Ser Leu Gln Asp Cys Ile Leu Asp Arg Asn Gln Ala Ala
 785 790 795 800
 Met Thr Val Leu Asn Gly His Val Val Val Cys Leu Phe Ala Asp Pro
 805 810 815
 Asp Ser Pro Leu Ile Gly Leu Arg Asn Leu Val Met Pro Leu Arg Ala
 820 825 830
 Ser Asn Phe His Tyr His Glu Leu Lys His Val Val Ile Val Gly Ser
 835 840 845
 Val Asp Tyr Ile Arg Arg Glu Trp Lys Met Leu Gln Asn Leu Pro Lys
 850 855 860
 Ile Ser Val Leu Asn Gly Ser Pro Leu Ser Arg Ala Asp Leu Arg Ala
 865 870 875 880
 Val Asn Val Asn Leu Cys Asp Met Cys Cys Ile Leu Ser Ala Lys Val
 885 890 895
 Pro Ser Asn Asp Asp Pro Thr Leu Ala Asp Lys Glu Ala Ile Leu Ala
 900 905 910
 Ser Leu Asn Ile Lys Ala Met Thr Phe Asp Asp Thr Ile Gly Val Leu
 915 920 925
 Ser Gln Arg Gly Pro Glu Phe Asp Asn Leu Ser Ala Thr Ala Gly Ser
 930 935 940
 Pro Ile Val Leu Gln Arg Arg Gly Ser Val Tyr Gly Ala Asn Val Pro
 945 950 955 960
 Met Ile Thr Glu Leu Val Asn Asp Gly Asn Val Gln Phe Leu Asp Gln
 965 970 975
 Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu Tyr Leu Thr Gln Pro Phe
 980 985 990

Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser
 995 1000 1005
 Thr Thr Tyr Phe Asn Gln Asn Ala Leu Thr Leu Ile Arg Ser Leu Ile
 1010 1015 1020
 Thr Gly Gly Ala Thr Pro Glu Leu Glu Leu Leu Ala Glu Gly Ala
 1025 1030 1035 1040
 Gly Leu Arg Gly Tyr Ser Thr Val Glu Ser Leu Ser Asn Arg Asp
 1045 1050 1055
 Arg Cys Arg Val Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln
 1060 1065 1070
 Phe Gly Glu Cys Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys
 1075 1080 1085
 Ser Tyr Gly Met Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser
 1090 1095 1100
 Ser Ser Cys Asp Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro
 1105 1110 1115 1120
 Asp Asp Phe Ser Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln
 1125 1130 1135
 Phe Asp Pro Gly Leu Glu Tyr Lys Pro Pro Ala Val Arg Ala Pro Ala
 1140 1145 1150
 Gly Gly Arg Gly Thr Asn Thr Gln Gly Ser Gly Val Gly Gly Gly
 1155 1160 1165
 Ser Asn Lys Asp Asp Asn Ser Leu Ser Asn Arg Asp Arg Cys Arg Val
 1170 1175 1180
 Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln Phe Gly Glu Cys
 1185 1190 1195 1200
 Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys Ser Tyr Gly Met
 1205 1210 1215
 Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser Ser Cys Asp
 1220 1225 1230
 Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro Asp Asp Phe Ser
 1235 1240 1245
 Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln Phe Asp
 1250 1255 1260

<210> 23
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense
 oligonucleotide

<400> 23
gtggatgata ccgacatgtt ggac

24

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense
oligonucleotide

<400> 24
gagaccacctt ctctccgtt tcgt

24

<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 (S4 to
S5) sense primer

<400> 25
ctcgaaactcc ctaaaatctt acagat

26

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 (S4 to
S5) antisense primer

<400> 26
ttccgtttag ccaggggtca ccagaatt

28

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 (S8 to
S9) sense primer

<400> 27
tctgctttgtt gaagctaaat ct

22

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 (S8 to
S9) antisense primer

<400> 28
tttcaaagcc tcttttagcgg taa

23

<210> 29
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 (S9 to
S10) sense primer

<400> 29
ttatgcctgg atctgcactc tacatg

26

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSlo3 (S9 to
S10) antisense primer

<400> 30
atagtttccg tctactaccg aaa

23

<210> 31
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:control human
beta-actin sense primer

<400> 31
gatgatatcg ccgcgcgtcg cgtcgac

27

<210> 32
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:control human
beta-actin antisense primer

<400> 32
tcggtccagg tctgcgtcct accgtac

27

<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:northern blot
sense primer

<400> 33
cgaaaaacgtc atgtacaatc gaaatcca

28

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:northern blot
antisense primer

<400> 34
ttccgttgag ccaggggtca ccagaatt

28

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human testis
cDNA library primer

<400> 35
ggcagcgctc attcttcct cctt

24

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human testis
cDNA library primer

<400> 36
tgcccaaaac ctcaacccaa aata

24

<210> 37
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region A peptide starting at amino acid 792

<400> 37
Ile Ala Val Asn
1

<210> 38
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region A peptide ending at amino acid 870

<400> 38
Leu Thr Glu Leu
1

<210> 39
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region A peptide starting at amino acid 793

<400> 39
Arg Ala Val Asn
1

<210> 40
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region A peptide ending at amino acid 885

<400> 40
Ile Thr Glu Leu
1

<210> 41
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region B peptide starting at amino acid 871

<400> 41
Lys Asn Pro Ser
1

<210> 42
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSl03 Region B peptide ending at amino acid 906

<400> 42
Gly Ala Val Phe
1

<210> 43
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSl01 Region B peptide starting at amino acid 886

<400> 43
Val Asn Asp Thr
1

<210> 44
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSl01 Region B peptide ending at amino acid 918

<400> 44
Gly Thr Ala Phe
1

<210> 45
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hybrid of mSl01
and mSl03 sequences at C-terminal end of chimera
Region B fragment

<400> 45
Gly Ala Ala Phe
1

<210> 46
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)...(4)
<223> mSlo3 Region C peptide starting at amino acid 899

<400> 46
Ser Thr Ser Phe
1

<210> 47
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)...(4)
<223> mSlo3 Region C peptide ending at amino acid 941

<400> 47
Ser Glu Met Glu
1

<210> 48
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)...(4)
<223> mSlo1 Region C peptide starting at amino acid 909

<400> 48
Thr Gln Pro Phe
1

<210> 49
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)...(4)
<223> mSlo1 Region C peptide ending at amino acid 963

<400> 49
Pro Glu Leu Glu
1

<210> 50
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region D peptide starting at amino acid 939

<400> 50
Glu Met Glu His
1

<210> 51
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region D peptide ending at amino acid 1034

<400> 51
His Leu Leu Pro
1

<210> 52
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region D peptide starting at amino acid 951

<400> 52
Glu Leu Glu Ala
1

<210> 53
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region D peptide ending at amino acid 1048

<400> 53
Glu Leu Val Pro
1